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piece 1, NC_000913, htrL_rfaD-, config: linear, direction: -, begin: 3792039, end: 3791687

[###> orf 7 codons

{-----} sd-(8)-ir 3791903 Gap 2.4 bits
|-----| sd-ir 3791903.htmL rfaD- total 10.4 bits

p35 6.1 bits

- ... p35-(22)-p10 3791873 Gap
- ... p35-p10 3791873 total 4.4

... -----} p35-(22)-p10 3791873 Gap 2.3 bits

... -----| p35-p10 3791873 total 4.4 bits

|-----| p35-p10_3791824 total 5.5 bits
 p35 6.2 bits p10 3.4 bits
 {-----} p35-(25)-p10_3791818

ap 4.0 bits
E 6 bits

{-----} p35-(26)-p10 3791817 Gap 3.7 bits
|-----| p35-p10 3791817 total 5.2 bits

p35 3.8 bits

{-----} p35-(21)-p10 3791805 Gap 3.3 bits
----- p35-p10 3791805 total 7.0 bits

The diagram illustrates the htrL-rfaD operon. It shows two promoters (green arrows) at the top, each followed by its respective gene sequence. The htrL promoter is associated with a sigma-70 factor (sd). The rfaD promoter is associated with a sigma-S factor (sd). Below the genes, a red box highlights the intergenic region (ir) between htrL and rfaD. A green box highlights the first 10 codons of the rfaD gene. Red dots indicate the start of translation for fMet at the first codon of rfaD and for ile at the 10th codon. A red arrow points to the 10 codon sequence as 'orf 10 codons'.

